



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 142739

TO: Nita M Minnifield
Location: REM-3C01&3C18
Art Unit: 1645
Wednesday, January 19, 2005

Case Serial Number: 10/030231

From: Mary Jane Ruhl
Location: Biotech-Chem Library
Remsen 1-A-62
Phone: 571-272-2524

maryjane.ruhl@uspto.gov

Search Notes

Examiner Minnifield,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl
Technical Information Specialist
STIC
Remsen 1-A-62
Ext. 22524

Reviewed
1-19-05
mm

142739

From: Chan, Christina
Sent: Tuesday, January 18, 2005 10:18 AM
To: Minnifield, Nita; STIC-Biotech/ChemLib
Subject: RE: rush interference sequence search

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

CRFE

-----Original Message-----

From: Minnifield, Nita
Sent: Friday, January 14, 2005 2:16 PM
To: Chan, Christina
Subject: rush interference sequence search

Christina, please approve, overdue AF amdt.

STIC

10/030231

Please do an interference sequence search on SEQ ID NO: 5, 6 and 7 of the above application.

Please provide a paper copy of the results.

Thanks,
Minnifield
71976
Art Unit 1645
Office REM-3C01
Mailbox REM-3C18

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search
NA Sequence: # _____
AA Sequence :# _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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OM protein - protein search, using sw model

Run on: January 18, 2005, 21:05:30 ; Search time 84.3333 Seconds
(without alignments)
171.363 Million cell updates/sec

Title: US-10-030-231-7
Perfect score: 251

Sequence: 1 HPHVCTSYCSKFCGCTGACCTGTCNHLHGKLCFLCHGR 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1608061 segs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/FCF_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	67	26.7	2164	US-10-123-155-151	Sequence 151, App
2	67	26.7	2164	US-10-146-721-151	Sequence 151, App
3	67	26.7	2164	US-10-140-472-151	Sequence 151, App
4	67	26.7	2164	US-10-141-761-151	Sequence 151, App
5	67	26.7	2164	US-10-142-885-151	Sequence 151, App
6	67	26.7	2164	US-10-158-790-151	Sequence 151, App
7	67	26.7	2164	US-10-137-871-151	Sequence 151, App
8	67	26.7	2164	US-10-140-923-151	Sequence 151, App
9	67	26.7	2164	US-10-141-756-151	Sequence 151, App
10	67	26.7	2164	US-10-141-759-151	Sequence 151, App
11	67	26.7	2164	US-10-140-805-151	Sequence 151, App
12	67	26.7	2164	US-10-140-864-151	Sequence 151, App
13	67	26.7	2164	US-10-142-426-151	Sequence 151, App

14	66	26.3	79	17	US-10-425-115-233868	Sequence 233868,
15	66	26.3	2849	14	US-10-123-155-285	Sequence 285, App
16	66	26.3	2849	14	US-10-146-731-285	Sequence 285, App
17	66	26.3	2849	14	US-10-140-472-285	Sequence 285, App
18	66	26.3	2849	14	US-10-141-761-285	Sequence 285, App
19	66	26.3	2849	14	US-10-142-885-285	Sequence 285, App
20	66	26.3	2849	14	US-10-158-790-285	Sequence 285, App
21	66	26.3	2849	14	US-10-137-871-285	Sequence 285, App
22	66	26.3	2849	14	US-10-140-923-285	Sequence 285, App
23	66	26.3	2849	14	US-10-141-756-285	Sequence 285, App
24	66	26.3	2849	14	US-10-141-759-285	Sequence 285, App
25	66	26.3	2849	14	US-10-140-805-285	Sequence 285, App
26	66	26.3	2849	14	US-10-140-864-285	Sequence 285, App
27	66	26.3	2849	15	US-10-142-426-285	Sequence 285, App
28	66	26.3	3240	14	US-10-184-644-415	Sequence 415, App
29	66	26.3	3240	14	US-10-184-644-415	Sequence 415, App
30	65.5	26.1	1371	14	US-10-123-155-487	Sequence 487, App
31	65.5	26.1	1371	14	US-10-146-731-487	Sequence 487, App
32	65.5	26.1	1371	14	US-10-140-472-487	Sequence 487, App
33	65.5	26.1	1371	14	US-10-141-761-487	Sequence 487, App
34	65.5	26.1	1371	14	US-10-142-885-487	Sequence 487, App
35	65.5	26.1	1371	14	US-10-158-790-487	Sequence 487, App
36	65.5	26.1	1371	14	US-10-137-871-487	Sequence 487, App
37	65.5	26.1	1371	14	US-10-140-923-487	Sequence 487, App
38	65.5	26.1	1371	14	US-10-141-756-487	Sequence 487, App
39	65.5	26.1	1371	14	US-10-141-759-487	Sequence 487, App
40	65.5	26.1	1371	14	US-10-140-805-487	Sequence 487, App
41	65.5	26.1	1371	14	US-10-140-864-487	Sequence 487, App
42	65.5	26.1	1371	15	US-10-142-426-487	Sequence 487, App
43	65	25.9	636	14	US-10-123-155-507	Sequence 507, App
44	65	25.9	636	14	US-10-146-731-507	Sequence 507, App
45	65	25.9	636	14	US-10-140-472-507	Sequence 507, App

ALIGNMENTS

RESULT 1
US-10-123-155-151
; Sequence 151, Application US/10123155
; General Information:
; Application No. US20030068794A1

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geo, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P33081C30
; CURRENT APPLICATION NUMBER: US/10/123,155
; PRIORITY FILING DATE: 2002-04-15
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 151
; LENGTH: 2164
; TYPE: DNA
; ORGANISM: Homo Sapien

Query Match 26.7%; Score 67; DB 14; Length 2164;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 18, 2005, 21:01:34 ; Search time 17.333 Seconds
(without alignments)
153,042 Million cell updates/sec

Title: US-10-030-231-7
Perfect score: 251

Sequence: 1 HPHVCTSYGSKFCGTAGCTRYGCRNLHGRKLCFCHCSR 40

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
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3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	64	25.5	109 2	US-08-527-044-2 Sequence 2, Appl1
2	64	25.5	109 3	US-09-013-780-2 Sequence 2, Appl1
3	63	25.1	430 3	US-08-997-897-2 Sequence 2, Appl1
4	63	25.1	430 3	US-09-156-836B-2 Sequence 2, Appl1
5	62	24.7	97 4	US-09-673-395A-384 Sequence 384, App
6	62	24.7	97 4	US-09-673-395A-411 Sequence 411, App
7	61.5	24.5	1342 1	US-07-978-895-4 Sequence 9, Appl1
8	61.5	24.5	1342 2	US-08-484-438-9 Sequence 4, Appl1
9	61.5	24.5	1342 2	US-08-473-119-4 Sequence 4, Appl1
10	61.5	24.5	1342 2	US-08-475-352-4 Sequence 4, Appl1
11	61.5	24.5	1342 2	US-09-170-699-4 Sequence 4, Appl1
12	61.5	24.5	1343 6	5183884-4 Patent No. 5183884
13	61	24.3	4	US-09-491-522-5 Sequence 3523, A
14	60	23.9	129 4	US-09-270-767-35232 Sequence 50449, A
15	60	23.9	129 4	US-09-270-767-50449 Sequence 10, Appl1
16	60	23.9	676 3	US-08-630-172-10 Sequence 10, Appl1
17	60	23.9	676 3	US-09-575-419-10 Sequence 1, Appl1
18	60	23.9	769 2	US-08-789-078-1 Sequence 1, Appl1
19	60	23.9	769 2	US-08-752-633-1 Sequence 45, Appl1
20	60	23.9	769 2	US-08-476-062A-45 Sequence 31, Appl1
21	60	23.9	769 2	US-07-728-215-31 Sequence 31, Appl1
22	60	23.9	769 3	US-08-938-085A-31 Sequence 31, Appl1
23	60	23.9	769 4	US-10-072-844-31 Sequence 31, Appl1
24	60	23.9	769 4	US-10-072-838-31 Sequence 31, Appl1
25	60	23.9	769 4	US-10-072-841A-31 Sequence 31, Appl1
26	60	23.9	769 4	US-10-219-631-31 Sequence 1, Appl1
27	60	23.9	769 5	PCT-US95-04866-1 Sequence 1, Appl1

28	60	23.9	769 5	PCT-US96-01314-45 Sequence 45, Appl1
29	59.5	23.7	147 4	US-09-252-991A-23465 Sequence 23465, A
30	59	23.5	969 4	US-09-321-987B-5 Sequence 5, Appl1
31	59	23.5	1205 4	US-09-491-522-11 Sequence 11, Appl1
32	59	23.5	2732 4	US-09-086-435-30 Sequence 30, Appl1
33	58.5	23.3	1345 2	US-08-977-767-3 Sequence 3, Appl1
34	58	23.1	70 3	US-09-188-930-131 Sequence 131, App
35	58	23.1	70 4	US-09-312-283C-131 Sequence 131, App
36	58	23.1	1064 4	US-09-270-767-45831 Sequence 45831, A
37	58	23.1	1193 2	US-08-400-159-10 Sequence 10, Appl1
38	58	23.1	1193 3	US-08-611-729A-10 Sequence 10, Appl1
39	58	23.1	1193 3	US-09-195-524-10 Sequence 10, Appl1
40	57.5	22.9	157 4	US-09-270-767-34570 Sequence 34570, A
41	57.5	22.9	157 4	US-09-270-767-49787 Sequence 49787, A
42	57.5	22.9	3460 3	US-09-334-220-1 Sequence 1, Appl1
43	57.5	22.9	3461 3	US-09-334-220-2 Sequence 2, Appl1
44	57	22.7	911 2	US-08-484-438-10 Sequence 10, Appl1
45	57	22.7	1058 2	US-08-484-438-4 Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-08-527-044-2

Sequence 2, Application US/08527044

Patent No. 5885568

GENERAL INFORMATION:

APPLICANT: BUNSTEAD, Janene Marilyn J.M.

APPLICANT: TOMLEY, Fiona Margaret F.

APPLICANT: DUNN, Patrick Paul James P.

APPLICANT: VERMEULEN, Arnoldus Nicolaas A.N.

TITLE OF INVENTION: Coccidiosis poultry vaccine

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSER: Akzo No. 5885568el N.V.

STREET: 1300 PICCARD DRIVE #206

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850-4373

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/527,044

FILING DATE: 12-SEP-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 94202667.6

FILING DATE: 16-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: GORMLEY, MARY E.

REGISTRATION NUMBER: 34,409

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 109 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULAR TYPE: protein

US-08-527-044-2

Query Match 25.5% Score 64; DB 2; Length 109;
Best Local Similarity 36.1%; Pred. No. 4;
Matches 13; Conservative 4; Mismatches 15; Indels 4; Gaps 1;
5 CTSYCSKFCGTAGCTRYGCRNLHGRKLCFCHCSR 40
40 CSTYCSKFCGSKCCSKCCSKCCNRRPSNRC---CSR 71

RESULT 2

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 18, 2005, 21:05:30 ; Search time 84.333 Seconds
(without alignments)
171.363 Million cell updates/sec

Title: US-10-030-231-6

Perfect score: 252

Sequence: 1 HSHACTSWCGKFCGTAAGCTHYLCRYLHPGKACVHCGR 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70.5	28.0	479	US-10-408-765A-1798	Sequence 1798, Ap
2	70.5	28.0	666	US-10-108-260A-4771	Sequence 4771, Ap
3	67.5	26.8	2119	US-10-123-155-61	Sequence 61, Appl
4	67.5	26.8	2119	US-10-146-731-61	Sequence 61, Appl
5	67.5	26.8	2119	US-10-140-472-61	Sequence 61, Appl
6	67.5	26.8	2119	US-10-141-761-61	Sequence 61, Appl
7	67.5	26.8	2119	US-10-142-885-61	Sequence 61, Appl
8	67.5	26.8	2119	US-10-158-790-61	Sequence 61, Appl
9	67.5	26.8	2119	US-10-137-871-61	Sequence 61, Appl
10	67.5	26.8	2119	US-10-140-923-61	Sequence 61, Appl
11	67.5	26.8	2119	US-10-141-756-61	Sequence 61, Appl
12	67.5	26.8	2119	US-10-141-759-61	Sequence 61, Appl
13	67.5	26.8	2119	US-10-140-805-61	Sequence 61, Appl

14	67.5	26.8	2119	US-10-140-864-61	Sequence 61, Appl
15	67.5	26.8	2119	US-10-142-426-61	Sequence 61, Appl
16	66	26.2	1162	US-10-123-155-185	Sequence 185, App
17	66	26.2	1162	US-10-146-731-185	Sequence 185, App
18	66	26.2	1162	US-10-140-472-185	Sequence 185, App
19	66	26.2	1162	US-10-141-761-185	Sequence 185, App
20	66	26.2	1162	US-10-142-885-185	Sequence 185, App
21	66	26.2	1162	US-10-158-790-185	Sequence 185, App
22	66	26.2	1162	US-10-137-871-185	Sequence 185, App
23	66	26.2	1162	US-10-140-923-185	Sequence 185, App
24	66	26.2	1162	US-10-141-766-185	Sequence 185, App
25	66	26.2	1162	US-10-141-759-185	Sequence 185, App
26	66	26.2	1162	US-10-140-805-185	Sequence 185, App
27	66	26.2	1162	US-10-140-864-185	Sequence 185, App
28	66	26.2	1162	US-10-142-885-185	Sequence 185, App
29	64.5	25.6	1371	US-10-123-155-487	Sequence 487, App
30	64.5	25.6	1371	US-10-146-731-487	Sequence 487, App
31	64.5	25.6	1371	US-10-140-472-487	Sequence 487, App
32	64.5	25.6	1371	US-10-141-761-487	Sequence 487, App
33	64.5	25.6	1371	US-10-142-885-487	Sequence 487, App
34	64.5	25.6	1371	US-10-158-790-487	Sequence 487, App
35	64.5	25.6	1371	US-10-137-871-487	Sequence 487, App
36	64.5	25.6	1371	US-10-140-923-487	Sequence 487, App
37	64.5	25.6	1371	US-10-141-756-487	Sequence 487, App
38	64.5	25.6	1371	US-10-141-759-487	Sequence 487, App
39	64.5	25.6	1371	US-10-140-805-487	Sequence 487, App
40	64.5	25.6	1371	US-10-140-864-487	Sequence 487, App
41	64.5	25.6	1371	US-10-142-885-487	Sequence 487, App
42	64.5	25.6	3608	US-10-184-644-433	Sequence 433, App
43	64.5	25.6	3608	US-10-184-634-433	Sequence 433, App
44	64.5	25.6	7285	US-10-145-206-28	Sequence 28, Appl
45	64	25.4	188	US-09-808-602-109	Sequence 109, App

ALIGNMENTS

RESULT 1
US-10-408-765A-1798
; Publication 1798, Application US/10408765A
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Brian D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660086.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1798
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1798

Query Match 28.0% Score 70.5; DB 16; Length 479;
Best Local Similarity 47.4% Pred. No. 15;
Matches 18; Conservative 2; Mismatches 13; Indels 5; Gaps 4;

QY 7 SYWCGKFCGTA--SCTHYLCR--VLAHGRK--CACHCSR 40
DB 121 AVEGCK--CGKAFKPSYLCRHEVTHSGKRCCECKCK 157

RESULT 2
US-10-108-260A-4771

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 18, 2005, 21:01:34 ; Search time 17.333 Seconds
(without alignments)
153.042 Million cell updates/sec

Title: US-10-030-231-6

Perfect score: 252

Sequence: 1 HSHACTSWGCKFCGTASTCTHYLCRVLPKQKACVHCSR 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 6631800 residues 478139

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
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3: /cgn2_6/prodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68	27.0	281	4	US-09-248-796A-15282
2	62.5	24.8	55	4	US-09-716-129-139
3	62	24.6	2732	4	US-09-086-436-30
4	61.5	24.4	1248	3	US-08-882-046-6
5	61.5	24.4	1248	4	US-09-566-047-6
6	60	23.8	1497	4	US-09-060-854B-2
7	59.5	23.6	125	4	US-09-270-767-38974
8	59.5	23.6	125	4	US-09-270-767-54191
9	59.5	23.6	1055	3	US-09-214-278-2
10	59.5	23.6	1055	4	US-09-855-722-2
11	59.5	23.6	1065	2	US-08-400-159-8
12	59.5	23.6	1148	3	US-08-882-046-4
13	59.5	23.6	1148	4	US-09-566-047-4
14	59.5	23.6	1212	3	US-09-214-278-3
15	59.5	23.6	1212	4	US-09-855-722-3
16	59.5	23.6	1238	3	US-09-214-278-5
17	59.5	23.6	1238	4	US-09-855-722-5
18	59.5	23.6	1257	3	US-08-611-729A-8
19	59.5	23.6	1257	4	US-09-195-524-8
20	59.5	23.6	1652	4	US-09-627-650B-1
21	59.5	23.6	1652	4	US-09-436-063C-1
22	59.5	23.6	1917	4	US-09-627-650B-5
23	59.5	23.6	2508	4	US-09-436-063C-5
24	59.5	23.6	2508	4	US-09-627-650B-7
25	59.5	23.6	2544	4	US-09-436-063C-7
26	59.5	23.6	2544	4	US-09-627-650B-3
27	59.5	23.6	2544	4	US-09-436-063C-3

28	59.5	23.6	2601	4	US-09-627-650B-9	Sequence 9, Appl1
29	59.5	23.6	2601	4	US-09-436-063C-9	Sequence 9, Appl1
30	58.5	23.2	262	4	US-09-252-991A-22359	Sequence 22359, A
31	58.5	23.2	965	4	US-09-538-092-650	Sequence 650, App
32	58	23.0	3075	2	US-08-460-309-5	Sequence 5, Appl1
33	58	23.0	3075	2	US-08-125-077-5	Sequence 5, Appl1
34	57.5	22.8	148	4	US-09-270-767-47174	Sequence 47174, A
35	57.5	22.8	187	4	US-09-673-395A-148	Sequence 148, App
36	57	22.6	90	4	US-09-419-381-90	Sequence 90, Appl1
37	57	22.6	133	4	US-09-612-033B-6	Sequence 6, Appl1
38	57	22.6	180	4	US-09-612-033B-10	Sequence 10, Appl1
39	57	22.6	198	4	US-09-612-033B-8	Sequence 8, Appl1
40	57	22.6	398	4	US-09-612-033B-14	Sequence 14, Appl1
41	57	22.6	696	4	US-08-933-711B-7	Sequence 7, Appl1
42	56.5	22.4	112	4	US-09-621-976-5911	Sequence 5911, Ap
43	56	22.2	109	2	US-08-527-044-2	Sequence 2, Appl1
44	56	22.2	109	2	US-09-013-780-2	Sequence 2, Appl1
45	56	22.2	356	4	US-09-054-272-18	Sequence 18, Appl1

ALIGNMENTS

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RESULT 1
US-09-248-796A-15282
; Sequence 15282, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15282
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-15282

Query Match      27.0%; Score 68; DB 4; Length 281;
Best Local Similarity 27.6%; Pred. No. 3.3;
Matches 16; Conservative 4; Mismatches 12; Indels 26; Gaps 3;

QY      9 WCGKFE-----CGT-----ASCTHYLCRVLPKQKAC-----VHCSR 40
DB      164 WCGKLINEPHNYLMPFGSCSMKNYKASCVHSCCTYICHPGQHPICGATGPMKCHCKGK 221

RESULT 2
US-09-716-129-139
; Sequence 139, Application US/09716129
; Patent No. 6632920
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 36 Human Secreted Proteins
; FILE REFERENCE: P202521
; CURRENT APPLICATION NUMBER: US/09/716,129
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/076,053
; PRIOR FILING DATE: 1998-02-26
; PRIOR APPLICATION NUMBER: 60/076,057
; PRIOR FILING DATE: 1998-02-26
; PRIOR APPLICATION NUMBER: 60/076,052
; PRIOR FILING DATE: 1998-02-26
; PRIOR APPLICATION NUMBER: 60/076,054
; PRIOR FILING DATE: 1998-02-26
; PRIOR APPLICATION NUMBER: 60/076,051
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OM protein - protein search, using sw model

Run on: January 18, 2005, 21:05:30 ; Search time 84.3333 Seconds
(without alignments)
171.363 Million cell updates/sec

Title: US-10-030-231-5

Perfect score: 199
Sequence: 1 HXHKTSYXCKKFCGTACTYXXCRXHXKXCKXHCGR 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66.5	33.4	479	US-10-408-765A-1798	Sequence 1798, App
2	66.5	33.4	666	US-10-108-260A-4771	Sequence 4771, App
3	66	33.2	2095	US-10-184-644-161	Sequence 161, App
4	66	33.2	2095	US-10-184-634-161	Sequence 161, App
5	66	33.2	2095	US-10-063-685-35	Sequence 35, App
6	65	32.7	2089	US-10-123-155-497	Sequence 497, App
7	65	32.7	2089	US-10-146-731-497	Sequence 497, App
8	65	32.7	2089	US-10-140-472-497	Sequence 497, App
9	65	32.7	2089	US-10-141-761-497	Sequence 497, App
10	65	32.7	2089	US-10-142-885-497	Sequence 497, App
11	65	32.7	2089	US-10-158-790-497	Sequence 497, App
12	65	32.7	2089	US-10-137-871-497	Sequence 497, App
13	65	32.7	2089	US-10-140-923-497	Sequence 497, App

14	65	32.7	2089	US-10-141-756-497	Sequence 497, App
15	65	32.7	2089	US-10-141-759-497	Sequence 497, App
16	65	32.7	2089	US-10-140-805-497	Sequence 497, App
17	65	32.7	2089	US-10-140-864-497	Sequence 497, App
18	65	32.7	2089	US-10-142-426-497	Sequence 497, App
19	63	31.7	2732	US-09-086-436-30	Sequence 30, App
20	63	31.7	2732	US-10-753-991-30	Sequence 30, App
21	63	31.7	2732	US-10-184-644-473	Sequence 473, App
22	63	31.7	2732	US-10-184-644-473	Sequence 473, App
23	63	31.7	2732	US-10-184-644-473	Sequence 473, App
24	63	31.7	2732	US-10-184-644-473	Sequence 473, App
25	63	31.7	2732	US-10-184-644-473	Sequence 473, App
26	63	31.7	2732	US-10-184-644-473	Sequence 473, App
27	62	31.2	1997	US-09-060-854B-2	Sequence 2, App
28	62	31.2	1997	US-10-029-217A-24	Sequence 24, App
29	61.5	30.9	3479	US-10-123-155-123	Sequence 123, App
30	61.5	30.9	3479	US-10-146-731-123	Sequence 123, App
31	61.5	30.9	3479	US-10-140-472-123	Sequence 123, App
32	61.5	30.9	3479	US-10-141-761-123	Sequence 123, App
33	61.5	30.9	3479	US-10-142-885-123	Sequence 123, App
34	61.5	30.9	3479	US-10-158-790-123	Sequence 123, App
35	61.5	30.9	3479	US-10-137-871-123	Sequence 123, App
36	61.5	30.9	3479	US-10-140-923-123	Sequence 123, App
37	61.5	30.9	3479	US-10-141-756-123	Sequence 123, App
38	61.5	30.9	3479	US-10-141-759-123	Sequence 123, App
39	61.5	30.9	3479	US-10-140-805-123	Sequence 123, App
40	61.5	30.9	3479	US-10-140-864-123	Sequence 123, App
41	61.5	30.9	3479	US-10-142-426-123	Sequence 123, App
42	61.5	30.9	3479	US-09-804-898-2	Sequence 2, App
43	61	30.7	636	US-10-123-155-507	Sequence 507, App
44	61	30.7	636	US-10-146-731-507	Sequence 507, App
45	61	30.7	636	US-10-140-472-507	Sequence 507, App

ALIGNMENTS

RESULT 1
US-10-408-765A-1798
; Sequence 1798, Application US//10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Bo D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1798
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1798

Query Match 33.4% Score 66.5; DB 16; Length 479;
Best Local Similarity 42.1%; Pred. No. 2.5; Mismatches 15; Gaps 4;
Matches 16; Conservative 2; Indels 5;

QY 7 SYXCKKFCGT-XCTYXCR-XLHXGX-CKXHCGR 40
DB 121 AVECTK-CGKAFKPSYLCRHVTHSGKPCCKCCK 157

RESULT 2
US-10-108-260A-4771

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 18, 2005, 21:01:34 ; Search time 17.3333 Seconds
(without alignments)
153.042 Million cell updates/sec

Title: US-10-030-231-5
Perfect score: 199
Sequence: 1 HXHCSTYCKKFCGTAACXYYXCRXHXGKXCXCHCSR 40

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues
Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/prodata/1/iaa/5A COMB pep.*
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3: /cgn2_6/prodata/1/iaa/6A COMB pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	31.7	2732	4	US-09-086-436-30 Sequence 30, Appl
2	62	31.2	1497	4	US-09-060-854B-2 Sequence 2, Appl
3	57	28.6	109	2	US-08-527-044-2 Sequence 2, Appl
4	57	28.6	109	3	US-09-013-780-2 Sequence 2, Appl
5	55	27.6	430	3	US-08-997-897-2 Sequence 2, Appl
6	55	27.6	430	3	US-09-156-836B-2 Sequence 2, Appl
7	55	27.6	1461	4	US-10-142-231-86 Sequence 86, Appl
8	55	27.6	2088	4	US-09-548-372D-13 Sequence 13, Appl
9	55	27.6	2088	4	US-09-548-367D-13 Sequence 13, Appl
10	55	27.6	2088	4	US-09-551-852D-13 Sequence 13, Appl
11	55	27.6	2088	4	US-09-548-376D-13 Sequence 13, Appl
12	55	27.6	2088	4	US-09-548-373D-13 Sequence 13, Appl
13	55	27.6	2088	4	US-09-548-366F-13 Sequence 13, Appl
14	54.5	27.4	1917	4	US-09-527-650B-5 Sequence 5, Appl
15	54.5	27.4	1917	4	US-09-436-063C-5 Sequence 5, Appl
16	54	27.1	281	4	US-09-252-991A-29199 Sequence 29199, A
17	53.5	26.9	55	4	US-09-716-129-139 Sequence 139, Appl
18	53.5	26.9	2508	4	US-09-627-650B-7 Sequence 7, Appl
19	53.5	26.9	2508	4	US-09-436-063C-7 Sequence 7, Appl
20	53.5	26.9	2544	4	US-09-627-650B-3 Sequence 3, Appl
21	53.5	26.9	2544	4	US-09-436-063C-3 Sequence 3, Appl
22	53.5	26.9	2601	4	US-09-627-650B-9 Sequence 9, Appl
23	53.5	26.9	2601	4	US-09-436-063C-9 Sequence 9, Appl
24	53	26.6	1388	4	US-09-463-048A-6 Sequence 6, Appl
25	53	26.6	1417	3	US-08-900-230-3 Sequence 3, Appl
26	51.5	25.9	908	4	US-08-714-741-44 Sequence 44, Appl
27	51.5	25.9	2211	3	US-09-738-884-1 Sequence 1, Appl

28	51.5	25.9	2211	4	US-10-096-961A-1	Sequence 1, Appl
29	50	25.1	90	4	US-09-419-381-90	Sequence 90, Appl
30	50	25.1	143	3	US-08-990-823-112	Sequence 112, Appl
31	50	25.1	143	4	US-09-477-135A-112	Sequence 112, Appl
32	50	25.1	1652	4	US-09-627-650B-1	Sequence 1, Appl
33	50	25.1	1652	4	US-09-436-063C-1	Sequence 1, Appl
34	49.5	24.9	1128	4	US-09-627-650B-11	Sequence 11, Appl
35	49.5	24.9	1128	4	US-09-436-063C-11	Sequence 11, Appl
36	49	24.6	379	1	US-08-468-847B-11	Sequence 11, Appl
37	49	24.6	379	4	US-09-142-569-2	Sequence 2, Appl
38	49	24.6	379	4	US-09-495-448-2	Sequence 2, Appl
39	49	24.6	717	4	US-09-644-460-37	Sequence 37, Appl
40	48.5	24.4	518	4	US-09-881-578A-4	Sequence 4, Appl
41	48	24.1	414	4	US-08-252-991A-31151	Sequence 31151, A
42	48	24.1	1400	3	US-08-630-915A-37	Sequence 37, Appl
43	48	24.1	1400	4	US-09-879-957-37	Sequence 37, Appl
44	47.5	23.9	138	4	US-09-270-767-39484	Sequence 39484, A
45	47.5	23.9	138	4	US-09-270-767-54701	Sequence 54701, A

ALIGNMENTS

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RESULT 1
US-09-086-436-30
Sequence 30, Application US/09086436
Patent No. 6703485
GENERAL INFORMATION:
APPLICANT: Kandell, Eric R.
APPLICANT: Santoro, Bina
APPLICANT: Bartsch, Dusan
APPLICANT: Siegelbaum, Steven
APPLICANT: Tibbs, Gareth
APPLICANT: Grant, Seth
TITLE OF INVENTION: Brain or Heart Cyclic Nucleotide Gated Ion Channel and
FILE REFERENCE: 0575/54806-A
CURRENT APPLICATION NUMBER: US/09/086,436
CURRENT FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
LENGTH: 2732
TYPE: PRT
ORGANISM: Murine
US-09-086-436-30

Query Match          31.7%; Score 63; DB 4; Length 2732;
Best Local Similarity 31.4%; Pred. No. 9.2;
Matches 11; Conservative 2; Mismatches 22; Indels 0; Gaps 0;

QY      5 CTSYXCKKFCGTAACXYYXCRXHXGKXCXCHCS 39
DB      2425 CCTCGAGCTTCTCTGCCCCATGAGTCTCCACT 2459

RESULT 2
US-09-060-854B-2
Sequence 2, Application US/09060854B
Patent No. 6642011
GENERAL INFORMATION:
APPLICANT: Estell, David Aaron
TITLE OF INVENTION: Human Protease and Use of Such Protease for Pharmaceutical
TITLE OF INVENTION: Applications and for Reducing the Allergenicity of No. 6642011-H
FILE REFERENCE: GC532
CURRENT APPLICATION NUMBER: US/09/060,854B
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1497
TYPE: PRT

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